

SEQUENCE LISTING

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SUZUKI, NORIKO
HANASAKI, KOHJI

<120> A GENE ENCODING NOVEL HUMAN SECRETORY TYPE PHOSPHOLIPASE A2

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<140> 10/088,092
<141> 2002-03-21

<150> PCT/JP00/06344
<151> 2000-09-18

<150> JP 11-266616
<151> 1999-09-21

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<170> PatentIn version 3.1

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cggtggctcc cactggccag tgggacgaaa cggattggtg ttgtcatgcc catgactgct 120
gctatggccg cctggagaaan ctgggctgtg accccaagct ggaaaagtac ctcttctcta 180
tcactcgaga caacatcttc tgtgctggta aaacggcttg ccagcggcat acctgcgaat 240
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agcttggttg ggtagtgggc 20

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 gggtgtaagt gttcagggtg tgg 23

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agggtggcaga gcaggctccc atgccccctg cctacctccc ccagg atg aaa cct ccc 177
Met Lys Pro Pro

att gcc ctg gct tgc ctt tgc ctc ctg gtg ccc ctg gct ggc ggg aac 225
Ile Ala Leu Ala Cys Leu Cys Leu Leu Val Pro Leu Ala Gly Gly Asn
-15 -10 -5 -1 1

ctg gtc cag ttt gga gtg atg att gag aga atg acg gga aag cct gcc 273
Leu Val Gln Phe Gly Val Met Ile Glu Arg Met Thr Gly Lys Pro Ala
5 10 15

ctg cag tac aat gac tat ggc tgc tat tgc ggt gtc ggt ggc tcc cac 321
Leu Gln Tyr Asn Asp Tyr Gly Cys Tyr Cys Gly Val Gly Gly Ser His
20 25 30

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tgg cca gtg gac gag acg gat tgg tgt tgt cat gcc cat gac tgc tgc	369
Trp Pro Val Asp Glu Thr Asp Trp Cys Cys His Ala His Asp Cys Cys	
35 40 45	
tat ggc cgc ctg gag aag ctg ggc tgt gac ccc aag ctg gaa aag tac	417
Tyr Gly Arg Leu Glu Lys Leu Gly Cys Asp Pro Lys Leu Glu Lys Tyr	
50 55 60 65	
ctc ttc tct atc act cga gac aac atc ttc tgt gct ggt aga acg gct	465
Leu Phe Ser Ile Thr Arg Asp Asn Ile Phe Cys Ala Gly Arg Thr Ala	
70 75 80	
tgc cag cgg cat acc tgc gag tgt gac aag aga gct gct ctt tgc ttt	513
Cys Gln Arg His Thr Cys Glu Cys Asp Lys Arg Ala Ala Leu Cys Phe	
85 90 95	
cgc cac aac ctg aac act tac aac cgc aag tat gcc cac tac ccc aac	561
Arg His Asn Leu Asn Thr Tyr Asn Arg Lys Tyr Ala His Tyr Pro Asn	
100 105 110	
aag ctg tgt act ggg ccc acc cca ccc tgc tgaggccctg ctcggtcca	611
Lys Leu Cys Thr Gly Pro Thr Pro Pro Cys	
115 120	
tagccacccc aggtgctgc agtctcaggc ccagagaagc tcggaaccca gattcctctc	671
ccagcagact catcccgccc cccccccaga gatcatgagc cctgggtctct ggctccagg	731
accacaccag atccacggga tcagctgaag aagtcacggg actcgtcagc gctcacaaga	791
tccactaagt cgcctctggc atctcaatac cctcttctga ataagagaag tctattttcc	851
cgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa	883

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Met Lys Pro Pro Ile Ala Leu Ala Cys Leu Cys Leu Leu Val Pro Leu
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Ala Gly Gly Asn Leu Val Gln Phe Gly Val Met Ile Glu Arg Met Thr
-1 1 5 10

Gly Lys Pro Ala Leu Gln Tyr Asn Asp Tyr Gly Cys Tyr Cys Gly Val
15 20 25

Gly Gly Ser His Trp Pro Val Asp Glu Thr Asp Trp Cys Cys His Ala
 30 35 40 45

His Asp Cys Cys Tyr Gly Arg Leu Glu Lys Leu Gly Cys Asp Pro Lys
 50 55 60

Leu Glu Lys Tyr Leu Phe Ser Ile Thr Arg Asp Asn Ile Phe Cys Ala
 65 70 75

Gly Arg Thr Ala Cys Gln Arg His Thr Cys Glu Cys Asp Lys Arg Ala
 80 85 90

Ala Leu Cys Phe Arg His Asn Leu Asn Thr Tyr Asn Arg Lys Tyr Ala
 95 100 105

His Tyr Pro Asn Lys Leu Cys Thr Gly Pro Thr Pro Pro Cys
 110 115 120

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tcctgggaga aggaggggaag cctgggggca cctggaaaat tcaggctgat ctctcctctg 180

ggctactttg ggctcgnggg ccccgagcag cccttggtcc agcccagcct ggctcacagg 240

tccctccagg tcaaccatga cccttgagg tgctgccacg cccacgactg ctgctacggg 300

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ctatggctgt tactgcggca tc 22

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ggcatcgggtg gctcccactg g 21

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21

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Met Lys Ser Pro His Val Leu Val Phe Leu Cys Leu Leu Val Ala Leu
          -15                      -10                      -5

gtc acc ggg aac ctg gtt cag ttt ggg gtg atg atc gag aag atg aca      154
Val Thr Gly Asn Leu Val Gln Phe Gly Val Met Ile Glu Lys Met Thr
          -1  1                      5                      10

ggc aag tcc gcc ctg cag tac aac gac tat ggc tgt tac tgc ggc atc      202
Gly Lys Ser Ala Leu Gln Tyr Asn Asp Tyr Gly Cys Tyr Cys Gly Ile
          15                      20                      25

ggg aag tcc cac tgg ccg gtg gac cag act gac tgg tgc tgc cac gcc      250
Gly Gly Ser His Trp Pro Val Asp Gln Thr Asp Trp Cys Cys His Ala
          30                      35                      40                      45

cac gac tgc tgc tac ggg cgt ctg gag aag ctg ggc tgt gag ccc aaa      298
His Asp Cys Cys Tyr Gly Arg Leu Glu Lys Leu Gly Cys Glu Pro Lys
          50                      55                      60

ctg gaa aag tat ctt ttc tct gtc agc gaa cgt ggc att ttc tgc gcc      346
Leu Glu Lys Tyr Leu Phe Ser Val Ser Glu Arg Gly Ile Phe Cys Ala
          65                      70                      75

ggc agg acc acc tgc cag cgg ctg acc tgc gag tgt gac aag agg gct      394
Gly Arg Thr Thr Cys Gln Arg Leu Thr Cys Glu Cys Asp Lys Arg Ala
          80                      85                      90

gcc ctc tgc ttt cgc cgc aac ctg ggc acc tac aac cgc aaa tat gcc      442
Ala Leu Cys Phe Arg Arg Asn Leu Gly Thr Tyr Asn Arg Lys Tyr Ala
          95                      100                      105

cat tat ccc aac aag ctg tgc acc ggg ccc acc ccg ccc tgc tga      487
His Tyr Pro Asn Lys Leu Cys Thr Gly Pro Thr Pro Pro Cys
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Met Lys Ser Pro His Val Leu Val Phe Leu Cys Leu Leu Val Ala Leu
          -15                      -10                      -5

Val Thr Gly Asn Leu Val Gln Phe Gly Val Met Ile Glu Lys Met Thr
          -1  1                      5                      10

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Gly Lys Ser Ala Leu Gln Tyr Asn Asp Tyr Gly Cys Tyr Cys Gly Ile
15 20 25

Gly Gly Ser His Trp Pro Val Asp Gln Thr Asp Trp Cys Cys His Ala
30 35 40 45

His Asp Cys Cys Tyr Gly Arg Leu Glu Lys Leu Gly Cys Glu Pro Lys
50 55 60

Leu Glu Lys Tyr Leu Phe Ser Val Ser Glu Arg Gly Ile Phe Cys Ala
65 70 75

Gly Arg Thr Thr Cys Gln Arg Leu Thr Cys Glu Cys Asp Lys Arg Ala
80 85 90

Ala Leu Cys Phe Arg Arg Asn Leu Gly Thr Tyr Asn Arg Lys Tyr Ala
95 100 105

His Tyr Pro Asn Lys Leu Cys Thr Gly Pro Thr Pro Pro Cys
110 115 120

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